

Figure 1

MKEIAMRNSKRKPEPTPFAGKKLRSTRRLRRKRAQISPVLVQSPPLWSKQIGVSAASVDSCS	60
DLLADDNVSCGSSRVEKSSNPCKTLIEEVEVSKPGYNVKETIGDSKFRRTITRSYKHLHKE	120
KEGDEIEVSESSCVDSNSGAGLRRLNVKGNKINDNEISFSRSDVTFAGHVSNSRSLNFE	180
SENKESDVSVISGVEYCSKFGSVTGGADNEEIEISKPSFVEADSSLGSAKELKPELEI	240
VGCVSDLACSEKFSEEVSDSLDDSESSEQRSEIYSQYSDFDYSDYTPSIFFDGSEFFSEKS	300
SSDSPISHRSRLYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRLRERE	360
RSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLS	420
<u>KGSFKSERTLILVGIASLTLATRIEENQPYNSIRKRNFTIQNLRYSRHEVVAMEWL</u> <u>VQEV</u>	480
<u>LNFKCFPTPTIFNFWFYLKAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALV</u> <u>VLA</u>	540
CIEHNKISAYQQRVIKVHVRTTDNELPECVKSLDWLLGQ	578

Figure 2

SDS 377 MDN-TGLIPRLRSIMVQWIVKQCSDMGLQQETFLGVGLLDRFLSKGSF 424  
 cyc2b MAQFDISDKMRAILIDWLVHDKFELMNETLFTVNLIDRFLSKQAV  
 cyc2a M-QQIDLNEKMRAILIDWLVHDKFELMNETLFTVNLIDRFLSKQNV  
 Consensus M + ++R+I++ W++ L +ETLFL+V L+DRFLSK

SDS 425 KSERTLILVGIASLTLATRIEE-NQPYNSIRKRNFTIQNLRYSRHEVVA 472  
 cyc2b -ARKKLQVLVGLVALLLACKYEEVSVV---IVEDLVVISDKAYTRTDVLE  
 cyc2a -MRKKLQVLVGLVALLLACKYEEVSVV---VVEDLVVISDKAYTRNDVLE  
 Consensus + L LVG+ +L LA + EE P + I Y+R +V+

SDS 473 MEWLVQEVINFKCFTPTIFNFWFLKAAARANPEVERKAKSLAVTSLSD 521  
 cyc2b MEKIMLSTLQFNMSLPTQYPFLKRFLKAAQSDKKLEILASFLIELALVD  
 cyc2a MEKIMLSTLQFNISLPTQYPFLKRFLKAAQADKKCEVLASFLIELALVE  
 Consensus ME - L+F PT + FL +LAAA A E A L +L D

Figure 3

	SDS	cyc2b	cyc2a	cyc3b	cycD
SDS	100%	34%/52%	34%/52%	28%/49%	21%/42%
cyc2b		100%	87%/92%	40%/60%	21%/43%
cyc2a			100%	46%/64%	22%/43%
cyc3b				100%	22%/41%